

Table IX. Starting alignments employed in model building

5	<p>1aba_: ----MFKVYGYDSNIHKCGPCD NAKRLL----TVKKQPFEFINI-MPEKGVFDDEKIAE--LLTKLGRDTQIG</p> <p>lego_: MQTV---IFGRS----GCPYCVRAKDLAEKLSN-ERDDFQYQYVDIRAEGI-TKEDLQQKA-----GKPVE--</p>
10	<p>1aba_: LTMPQVFAPD GSHIGGFDQLREYFK-----</p> <p>lego_: -TVPQIFV-DQQHIGGYTDFAAWVKENLDA</p>
15	<p>1bbhA: --AGLSPEEQIETR----QAGYEFMG---WNMGKIKANLEGEYNAAQVEAAANVIAAIA NSGMGALYGPG-TD</p> <p>2ccyA: QS---KPEDLLKLRQGLMQTLKSQWVPIAGFAAGKADLPADAAQRAENMAMVAKLAPIGWAKGTEAL-PNG--</p>
20	<p>1bbhA: KNVGDVKTRVKPEFFQN--MEDVGKIAREFVGAANTLA EVAATGEAEAVKTAFGDVGAACKSCHEKYRAK</p> <p>2ccyA: -----ETKPEAFGSKS-AEFLEGWKALATESTKLAAA AKAGP-DALKAQAAATGKVCKACHEEFKQD</p>
25	<p>1cewI: -----GAPVPVDE-NDEGLQRALQFAM-AEYNRASNDKYS-SRVVRVISA-----KRQLVSGIK-YILQV--</p> <p>1molA: GEWEI---IDIGPF----TQNLGKFAVDEENKIGQYGR LTFNKVIRPCMKKTIYENERE----IKGYEYQLYV</p>
30	<p>1cewI: EIGRTTC PKSSGDLQSCEF----HDEPEMAKYTTCTFVVYSIP---WLNQIKLLESKCQ--</p> <p>1molA: Y-----ASDKLFRADISEY-----KTRGRKLLRFNGPV-----PPP</p>

5	<p>1hom_: MRKRGRQTYTRYQTLEL----EKEFHFNRYLTRRRR----- IEIAHALC-----L</p> <p>11fb_: -----RFKWGPAS-QQI-LFQAYERQKNPSKEERETLVE- ECNRAECZQRGVSPSQAQGLGSNLV</p> <p>1hom_: TERQIKIWFQNRMRMKWKKENKTKGEPG</p> <p>11fb_: TEVRVYNWFANR---RKEEAFRH----</p>
10	<p>2pcy_: ---IDVLLGADDGSLAFVPSEFSISPGEKIVEK----- NNAGFPHNIVFDEDSIPSGVDASKISMSE</p> <p>2azaA: AQC-EATIESND-AMQYDLKEMVVDKSCK- QFTVHLKHVGKMAKSAMG--HNWVLTKEADKEGVATDGMNAGL</p>
15	<p>2pcy_: EDLLNA-----KGETFEVAL-----SNKGEYSFY- CSPHQGAGMVGKVTVN--</p> <p>2azaA: AQDYVKAGDTRVIAHTKVIGGGESDSVTFDVSKLTPGEAYAYFCSFPGHWA MMKGTLKL-SN</p>
20	<p>1stfl: -MMSGAPSATQPATAETQ-HIADQV-RSQLEE-KYNKK-FPV- FKAVSFK-----SQVVAGTNYFIKVHVGDE</p> <p>1mola: G----- EWEIIDIGPFTQNLGKFAVDEENKIGQYGRLTfNKVIRPCMKKTTYENEREIK G-YEYQLYVYAS</p> <p>1stfl: DfVHLRVFQSLPHENKPLTLsNYQTNKAKHDELTYF</p> <p>1mola: DKLFRADI-SEDYKTRGRKLLRF---NGPVPPP---</p>
25	<p>1tlk_: VAEKPHVKPYFTKTLDM-----VVEGSAARFDCKVEGY-----P----- -DPEVMWFKDDNPVKES</p> <p>2rhe_: -----ESVLTQPPSASGT-- PGQRVTISCTGSATDIGSNSVIWYQQVPGKAPKLLIYYNDLLPSG</p> <p>1tlk_: -RHFQIDYDEEGNCSLTISEVCGDDDAKYTCKAVNSLGEAT----- CTAELLVETM--</p>
30	<p>2rhe_: VSDRFSASKSGTSASLAISGLESEDEADYYCAAWNDLDEPGFGGG-- -TKLTVLGQPK-</p>

5

256bA: --ADLEDNMETLNDNLKV-----
IEKADNAAQVKDALTKMRAAALDAQKAT-PPKLEDKSPD-S---

1bbhA:
AGLSPEEQIETRQAGYEFMGWNMGKIKANLEGEYNAAQVEAAANVIAAIA
NSGMGALYGPGETDKNVGDVKTRV

10

256bA_: -PEMKDFRHGFDIL-----
VGQIDDALKLANEGKVKEAQAAAEQLKTTRNAYHQKYR--

1bbhA: KPEF--
FQNMEDVGKIAREFVGAANTLAEVAATGEAEAVKTAFGDVGAACKSCHEK
YRAK

15

2azaA:
AQCEATIESNDAMQYDLKEMVVDKSCQFTVHLKHVKGMAKSAM-----
GHNWVLTKEADKEG-----VATDG

1paz_: -----ENIEVHM--LNKGAEGAMVFEP--YI---
KANPGDVTFTIPVDKG

2azaA: MNAGLAQDYVKAGDTRV-
IAHTKVIGGGESDSVTFDVSKLTPGEAYAYFCS-FPGHWA--MMKGTLKLSN-
--

20

1paz_: HNVESIKDMIPEGAEKFK-----SKINENYVLTVTQ--PG-AYLVKCTP-
--HYAMGMI-ALIAVGDSPA

2azaA: -----

1paz_: NLDQIVSAKKPKIVQERLEK VIA

25

2sarA: -----DVSGTVCLSALPPEATDTLNLIAS-DGPFPPYSQDGV-----
VFQNRRESVLPTQSYGYYHEY

9rnt_: ACDYTCGSNCYSS-----SDVSTAQAAGYKL---HEDGETVGSNSY-
PHKYN NYEGFDFSVSSPYY

2sarA: TV-----ITPGARTRGTRRIICGEATQEDYYTGDHYATFS---LIDQTC-
-

30

9rnt_: EWPILSSGDVY--SGGSPGADR VVFN---ENNQLAGVITHTGASGNN--
FVECT-